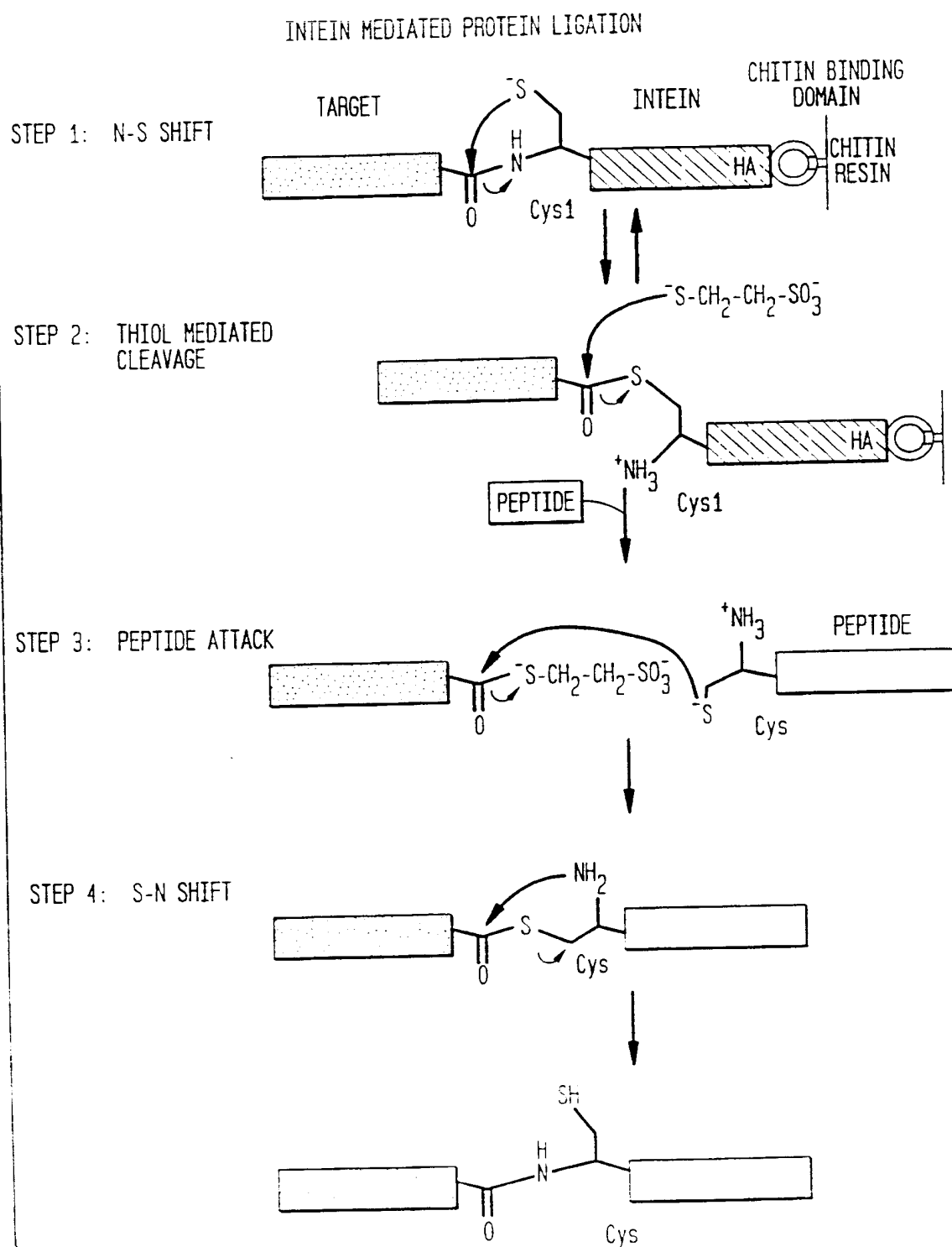


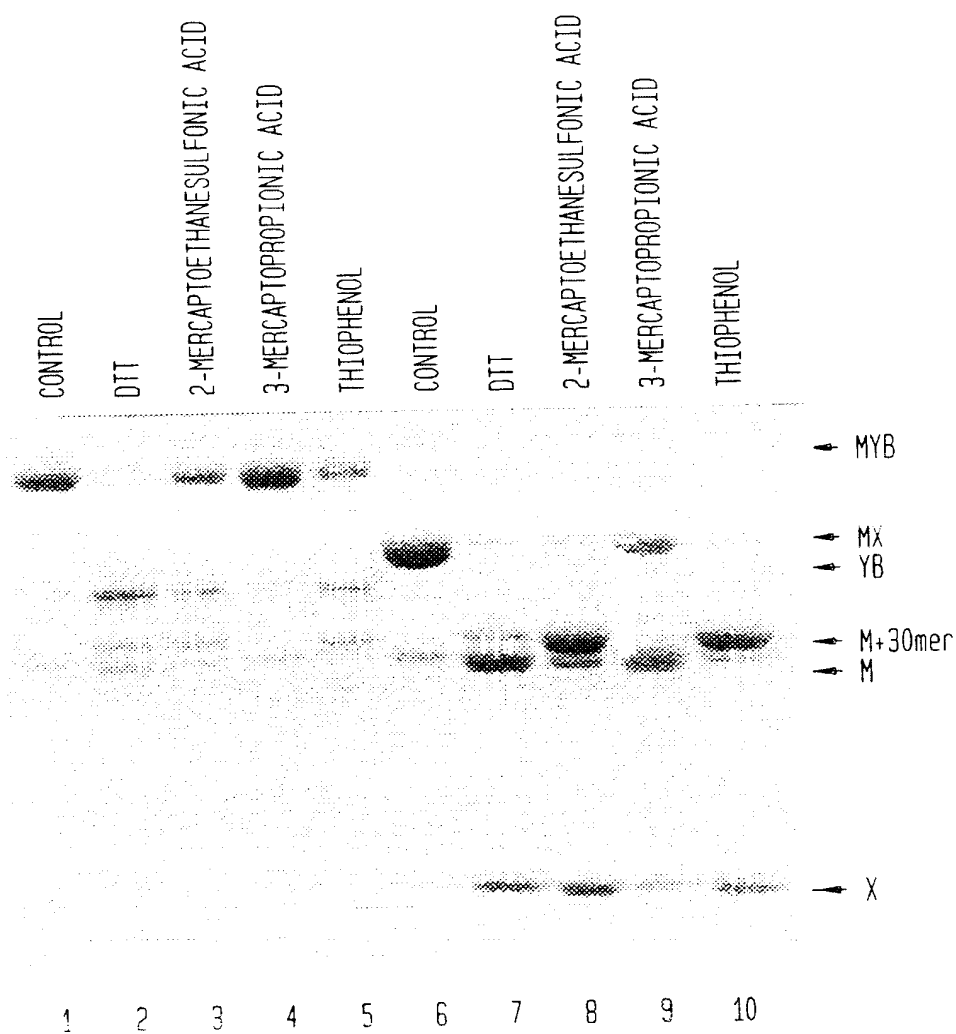
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FIG. 1



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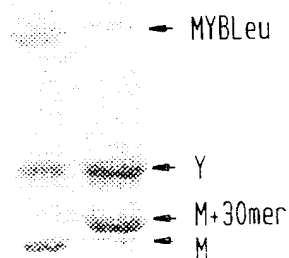
FIG. 2



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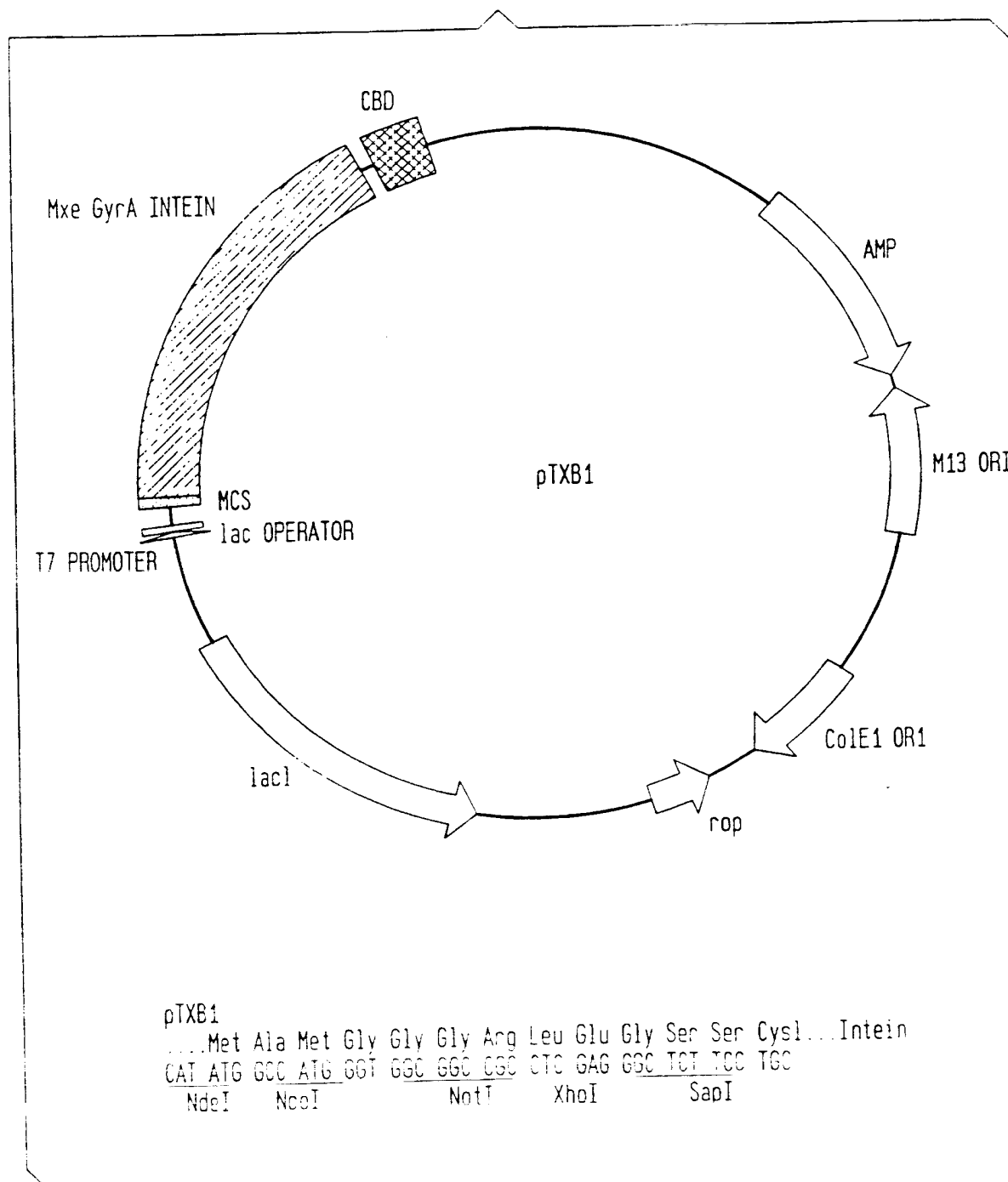
FIG. 3

DIRECT LIGATION REACTION



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FIG. 4



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FIG. 5A

DNA Sequence of pTXB1 plasmid

140- 997 beta-lactamase (Ap)
1042-1555 M13 origin
2254 ColE1 origin
2626-2814 rop
3376-4455 lacIq
5440-5456 T7 promoter
5440-5459 T7 universal primer (forward)
5457 first nucleotide of the T7 transcript
5459-5483 lac operator
5513-5519 Shine-Dalgarno sequence (T7 gene 10)
5525-5572 Multiple cloning site
5573-6166 Mxe GyrA intein (N198A)
6197-6352 Chitin-binding domain
6375-6497 T7 transcription terminator

TXB1.seq.old Length: 6503 March 17, 1998 11:14 Type: N
Check: 1445 ..

1 AACTACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT
51 GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA
101 CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA
151 ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TCGGCGCATTT TGCCTTCCTG
201 TTTTGTCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG
251 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT
301 CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA
351 AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGTTGACGC CGGGCAAGAG
401 CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC
451 ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT
501 GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG
551 ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG
601 GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA
651 TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG
701 TTGCGCAAAC TATTAAGTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA
751 ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT
801 CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG
851 CGTGGGTCTC GCGSTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC

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FIG. 5B

901 CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
951 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA
1001 CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TACCCCGGTT
1051 GATAATCAGA AAAGCCCCAA AAACAGGAAG ATTGTATAAG CAAATATTTA
1101 AATTGTAAAC GTTAATATTT TGTTAAAATT CGCGTTAAAT TTTTGTAA
1151 TCAGCTCATT TTTTAACCA TAGGCCGAAA TCGGCAAAAT CCGTTATAAA
1201 TCAAAAGAAT AGCCCGAGAT AGGGTTGAGT GTTGTTCAG TTTGGAACAA
1251 GAGTCCACTA TTAAAGAACG TGGACTCCAA CGTCAAAGG CGAAAAACCG
1301 TCTATCAGGG CGATGGCCCA CTACGTGAAC CATCACCCAA ATCAAGTTTT
1351 TTGGGGTCGA GGTGCCGTAA AGCACTAAAT CGGAACCCTA AAGGGAGCCC
1401 CCGATTTAGA GCTTGACGGG GAAAGCCGGC GAACGTGGCG AGAAAGGAAG
1451 GGAAGAAAGC GAAAGGAGCG GCGCTAGGG CGCTGGCAAG TGTAGCGGTC
1501 ACGCTGCGCG TAACCACCAC ACCCGCCGCG CTTAATGCGC CGCTACAGGG
1551 CGCGTAAAG GATCTAGGTG AAGATCCTTT TTGATAATCT CATGACCAA
1601 ATCCCTTAAC GTGAGTTTTT GTTCCACTGA GCGTCAGACC CCGTAGAAAA
1651 GATCAAAGGA TCTTCTTGAG ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT
1701 TGCAAACAAA AAAACCACCG CTACCAGCGG TGGTTTGTTT GCCGGATCAA
1751 GAGCTACCAA CTCTTTTTTC GAAGGTAAGT GGCTTCAGCA GAGCGCAGAT
1801 ACCAAATACT GTCCTTCTAG TGTAGCCGTA GTTAGGCCAC CACTTCAAGA
1851 ACTCTGTAGC ACCGCCTACA TACCTCGCTC TGCTAATCCT GTTACCAGTG
1901 GCTGCTGCCA GTGGCGATAA GTCGTGTCTT ACCGGGTTGG ACTCAAGACG
1951 ATAGTTACCG GATAAGGCGC AGCGGTCGGG CTGAACGGGG GGTTTCGTGCA
2001 CACAGCCCAG CTTGGAGCGA ACGACCTACA CCGAACTGAG ATACCTACAG
2051 CGTGAGCTAT GAGAAAGCGC CACGCTTCCC GAAGGGAGAA AGGCGGACAG
2101 GATCCCGTA AGCGGCAGGG TCGGAACAGG AGAGGGGAGG AGGGAGCTTC
2151 CAGGGGGAAA CGCCTGGTAT CTTTATAGTC CTGTCGGSTT TCGCCACCTC
2201 TGAATTGAGC GTCGATTTTT GTGATGCTCG TCAGGGGGGC GGAGCCTATG
2251 GAAAAACGCC AGCAACGCGG CCTTTTTACG GTTCCTGGCC TTTTGCTGGC
2301 CTTTGCTCA CATGTTCTTT CCGCGTTAT CCGCTGATTC TGTGGATAAC

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FIG. 5C

2351 CGTATTACCG CCTTTGAGTG AGCTGATACC GCTCGCCGCA GCCGAACGAC
2401 CGAGCGCAGC GAGTCAGTGA GCGAGGAAGC TATGGTGCAC TCTCAGTACA
2451 ATCTGCTCTG ATGCCGCATA GTTAAGCCAG TATACACTCC GCTATCGCTA
2501 CGTGACTGGG TCATGGCTGC GCCCCGACAC CCGCCAACAC CCGCTGACGC
2551 GCCCTGACGG GCTTGTCTGC TCCCGGCATC CGCTTACAGA CAAGCTGTGA
2601 CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTACCGTC ATCACCAGAA
2651 CGCGCGAGGC AGCTGCGGTA AAGCTCATCA GCGTGGTCGT GCAGCGATTG
2701 ACAGATGTCT GCCTGTTTAT CCGCGTCCAG CTCGTTGAGT TTCTCCAGAA
2751 GCGTTAATGT CTGGCTTCTG ATAAAGCGGG CCATGTTAAG GGCGGTTTTT
2801 TCCTGTTTGG TCACTTGATG CCTCCGTGTA AGGGGGAATT TCTGTTTATG
2851 GGGGTAATGA TACCGATGAA ACGAGAGAGG ATGCTCACGA TACGGGTTAC
2901 TGATGATGAA CATGCCCGGT TACTGGAACG TTGTGAGGGT AAACAACTGG
2951 CGGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG TCAATGCCag
3001 ccgaACGCCA GCAAGACGTA GCCCAGCGCG TCGGCCGCCA TGCCGGCGAT
3051 AATGGCCTGC TTCTCGCCGA AACGTTTGGT GGCGGGACCA GTGACGAAGG
3101 CTTGAGCGAG GCGGTGCAAG ATTCCGAATA CCGCAAGCGA CAGGCCGATC
3151 ATCGTCGCGC TCCAGCGAAA GCGGTCCTCG CCGAAAATGA CCCAGAGCGC
3201 TGCCGGCACC TGTCTTACGA GTTGCATGAT AAAGAAGACA GTCATÁAGTG
3251 CGGCGACGAT AGTCATGCCC CGCGCCCACC GGAAGGAGCT GACTGGGTTG
3301 AAGGCTCTCA AGGGCATCGG TCGAGATCCC GGTGCCTAAT GAGTGAGCTA
3351 ACTTACATTA ATTGCGTTGC GCTCACTGCC CGCTTTCCAG TCGGGAAACC
3401 TGTCTGTCCA GCTGCATTAA TGAATCGGCC AACGCGCGGG GAGAGGCGGT
3451 TTGCGTATTG GGCGCCAGGG TGSTTTTTCT TTTCACCACT GAGACGGGCA
3501 ACAGCTGATT GCCCTTCACC GCCTGGCCCT GAGAGAGTTG CAGCAAGCGG
3551 TCCACGCTGG TTTGCCCCAG CAGGCGAAAA TCCTGTTTGA TGSTGTTAA
3601 CGGCGGGATA TAACATGAGC TGTCTTCGGT ATCGTCGTAT CCCACTACCG
3651 AGATATCCGC ACCAACCGCG AGCCCGGACT CGGTAATGGC GCGCATTGGC
3701 CCCAGCGCCA TCTGATCGTT GGCAACCAGC ATCGCAGTGG GAACGATGCC
3751 CTCATTCAGC ATTTGCATGG TTTGTTGAAA ACCGGACATG GCACTCCAGT

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FIG. 5D

3801 CGCCTTCCCG TTCCGCTATC GGCTGAATTT GATTGCGAGT GAGATATTTA
3851 TGCCAGCCAG CCAGACGCAG ACGCGCCGAG ACAGAACTTA ATGGGCCCCG
3901 TAACAGCGCG ATTTGCTGGT GACCCAATGC GACCAGATGC TCCACGCCCA
3951 GTCGCGTACC GTCTTCATGG GAGAAAATAA TACTGTTGAT GGGTGTCTGG
4001 TCAGAGACAT CAAGAAATAA CGCCGGAACA TTAGTGCAGG CAGCTTCCAC
4051 AGCAATGGCA TCCTGGTCAT CCAGCGGATA GTTAATGATC AGCCCACTGA
4101 CGCGTTGCGC GAGAAGATTG TGCACCGCCG CTTTACAGGC TTCGACGCCG
4151 CTTGTTCTA CCATCGACAC CACCACGCTG GCACCCAGTT GATCGGCGCG
4201 AGATTTAATC GCCGCGACAA TTTGCGACGG CGCGTGCAGG GCCAGACTGG
4251 AGGTGGCAAC GCCAATCAGC AACGACTGTT TGCCCGCCAG TTGTTGTGCC
4301 ACGCGGTTGG GAATGTAATT CAGCTCCGCC ATCGCCGCTT CCACTTTTTC
4351 CCGCGTTTTT GCAGAAACGT GGCTGGCCTG GTTACCACG CGGGAAACGG
4401 TCTGATAAGA GACACCGGCA TACTCTGCGA CATCGTATAA CGTTACTGGT
4451 TTCACATTCA CCACCCTGAA TTGACTCTCT TCCGGGCGCT ATCATGCCAT
4501 ACCGCGAAAG GTTTTGCGCC ATTGATGGT GTCCCGGATC TCGACGCTCT
4551 CCCTTATGCG ACTCCTGCAT TAGGAAGCAG CCCAGTAGTA GGTGAGGCC
4601 GTTGAGCACC GCCGCCGCAA GGAATGGTGC ATGCCGCCCT TTCGTCTTCA
4651 AGAATTAATT CCCAATTCCA GGCATCAAAT AAAACGAAAG GCTCAGTCGA
4701 AAGACTGGGC CTTTCGTTTT ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG
4751 AGTAGGACAA ATCCGCCGGG AGCGGATTTG AACGTTGCGA AGCAACGGCC
4801 CGGAGGGTGG CGGGCAGGAC GCCCCCATA AACTGCCAGG AATTAATTCC
4851 AGGCATCAA TAAAACGAAA GGCTCAGTCG AAAGACTGGG CCTTTCGTTT
4901 TATCTGTTGT TTGTGCGTGA ACGCTCTCCT GAGTAGGACA AATCCGCCGG
4951 GAGCGGATTT GAACGTTGCG AAGCAACGCG CCGGAGGGTG GCGGGCAGGA
5001 CGCCCCCAT AACTGCCAG GAATTAATTC CAGGCATCAA ATAAAACGAA
5051 AGGCTCAGTC GAAAGACTGG GCCTTTCGTT TTATCTGTTG TTTGTGGTG
5101 AACGCTCTCC TGAGTAGGAC AAATCCGCCG GGAGCGGATT TGAACGTTGC
5151 GAAGCAACGG CCCGGAGGGT GGCGGGCAGG ACGCCCGCCA TAACTGCCA
5201 GGAATTAATT CCAGGCATCA AATAAACGA AAGGCTCAGT CGAAAGACTG

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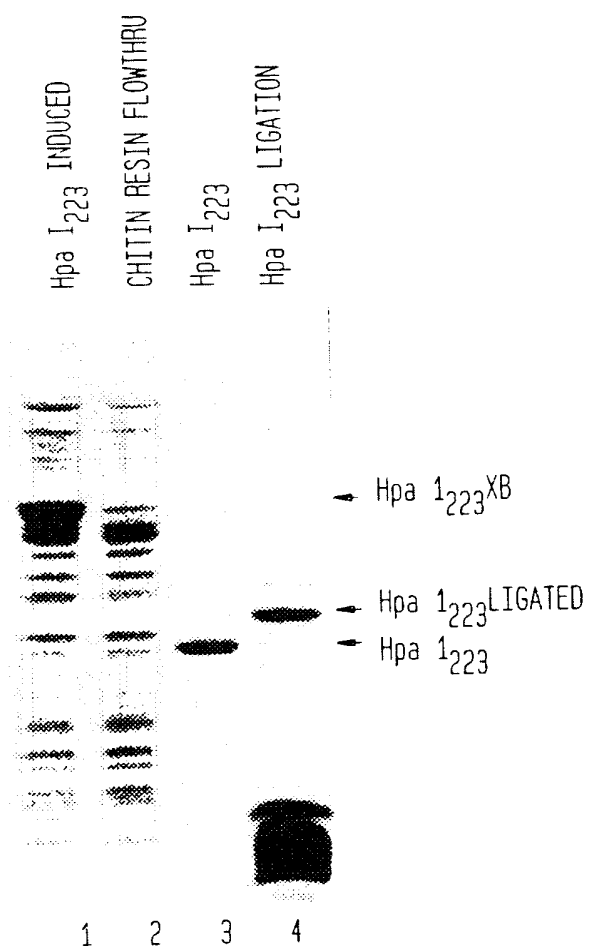
FIG. 5E

5251 GGCCTTTCGT TTTATCTGTT GTTTGTCGGT GAACGCTCTC CTGAGTAGGA
5301 CAAATCCGCC GGGAGCGGAT TTGAACGTTG CGAAGCAACG GCCCGGAGGG
5351 TGGCGGGCAG GACGCCCCGCC ATAAACTGCC AGGAATTGGG GATCGGAATT
5401 AATTCCCGGT TTAAACCGGG GATCTCGATC CCGCGAAATT AATACGACTC
5451 ACTATAGGGG AATTGTGAGC GGATAACAAT TCCCCTCTAG AAATAATTTT
5501 GTTTAACTTT AAGAAGGAGA TATAcatatg gctagctcgc gagtcgacgg
5551 cggccgcctc gagggctctt cctGCATCAC GGGAGATGCA CTAGTTGCCC
5601 TACCCGAGGG CGAGTCGGTA CGCATCGCCG ACATCGTGCC GGGTGCGCGG
5651 CCCAACAGTG ACAACGCCAT CGACCTGAAA GTCCTTGACC GGCATGGCAA
5701 TCCCGTGCTC GCCGACCGGC TGTTCCTCTC CGGCGAGCAT CCGGTGTACA
5751 CGGTGCGTAC GGTCTGAAGGT CTGCGTGTGA CGGGCACCGC GAACCACCCG
5801 TTGTTGTGTT TGGTCGACGT CGCCGGGGTG CCGACCCTGC TGTGGAAGCT
5851 GATCGACGAA ATCAAGCCGG GCGATTACGC GGTGATTCAA CGCAGCGCAT
5901 TCAGCGTCGA CTGTGCAGGT TTTGCCCCGG GAAAACCCGA ATTTGCGCCC
5951 ACAACCTACA CAGTCGGCGT CCCTGGACTG GTGCGTTTCT TGGAAGCACA
6001 CCACCGAGAC CCGGACGCCC AAGCTATCGC CGACGAGCTG ACCGACGGGC
6051 GGTCTACTA CGCGAAAGTC GCCAGTGTC ACGACGCCGG CGTGACGCCG
6101 GTGTATAGCC TTCGTGTGCA CACGGCAGAC CACGCGTTTA TCACGAACGG
6151 GTTCGTCAGC CACGCTACTG GCCTCACC GG TCTGAACTCA GGCCTCACGA
6201 CAAATCCTGG TGTATCCGCT TGGCAGGTCA ACACAGCTTA TACTGCGGGA
6251 CAATTGGTCA CATATAACGG CAAGACGTAT AAATGTTTGC AGCCCCACAC
6301 CTCCTTGGCA GGATGGGAAC CATCCAACGT TCCTGCCTTG TGGCAGCTTC
6351 AATGActgca ggaaggGGAT CCGGCTGCTA ACAAAGCCCC AAAGGAAGCT
6401 GAGTTGGCTG CTGCCACCGC TGAGCAATAA CTAGCATAAC CCGTTGGGGC
6451 CTCTAAACGG GTCTTGAGGG GTTTTTTGT GAAAGGAGGA ACTATATCCG
6501 GAT

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FIG. 6

Hpa I LIGATION



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FIG. 7

WESTERN BLOTS OF PROTEINS LIGATED TO A BIOTINYLATED PEPTIDE

